RAW SEQUENCE LISTING
ERROR REPORT
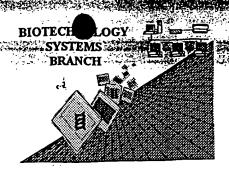
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/782,8/6_

Source: _OIPE_

Date Processed by STIC: _6/19/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov **or phone 703-306-4119 (R. Wax)**
PATENTIN 3.0 e-mail help: patin3help@uspto.gov **or phone 703-306-4119 (R. Wax)**

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _09/782,8/6_

1 ___ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
___ Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
prevent "wrapping."

2 ___ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
Numbering   use space characters, instead.

4 ___ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length   Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
each n or Xaa can only represent a single residue. Please present the maximum number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ___ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
"bug"   sequences(s) ___. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.

7 ___ Skipped Sequences   Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence:
(OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ___ Skipped Sequences   Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence.
(NEW RULES)   <210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ___ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
is Artificial Sequence

11 ___ Use of <220>   Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
"Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

AMC – Biotechnology Systems Branch – 06/04/2001

RAW SEQUENCE LISTING   DATE: 06/19/2001
PATENT APPLICATION: **US/09/782,816**   TIME: 12:05:17

Input Set : **A:\PTO.txt**
Output Set: **N:\CRF3\06192001\I782816.raw**

```
    4 <110> APPLICANT: Sharp, David J.
    5          Rogers, Gregory C.
    6          Scholey, Jonathon M.
    8 <120> TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
    9          PROLIFERATION
   11 <130> FILE REFERENCE: UC069.001A
   13 <140> CURRENT APPLICATION NUMBER: 09/782,816
C--> 14 <141> CURRENT FILING DATE: 2001-06-04
   16 <160> NUMBER OF SEQ ID NOS: 56
   18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
```

ERRORED SEQUENCES

```
  898 <210> SEQ ID NO: 56
  899 <211> LENGTH: 380
  900 <212> TYPE: PRT
  901 <213> ORGANISM: Drosophila melanogaster
  903 <400> SEQUENCE: 56
  904 Met Ala Asp Pro Lys Phe Gln Asn Leu Pro Gly Ile Ala Tyr Asp Gln
  905 1               5                   10                  15
  906 Pro Asp Val Tyr Glu Thr Pro Asp Asp Pro Glu Leu Asp Thr Ser Asp
  907             20                  25                  30
  908 Tyr Tyr Glu Glu Glu Pro Glu Asn Glu Ala Ile Glu Arg Leu His Ile
  909         35                  40                  45
  910 Ser Pro Ser Val Ala His Lys Arg Phe Ser Gly Ala Thr Val Glu Gly
  911     50              .       55                  60
  912 Ser Val Asp Phe Thr Asp Arg Ile Gly Arg Arg Met Cys Arg Gly Tyr
  913 65                  70                  75                  80
  914 Asp Thr Arg Gly Ser Ser Asp Tyr Glu Leu Val Gly Gln Gly Glu Lys
  915             85                  90                  95
  916 Glu Thr Pro Val Gln Lys Cys Gln Arg Leu Gln Ile Glu Met Asn Glu
  917             100                 105                 110
  918 Leu Leu Asn Glu Val Ala Ala Leu Gln Val Asp Arg Lys Val Ala Asp
  919         115                 120                 125
  920 Glu Glu Lys Gln Ser Tyr Asp Ala Val Ala Thr Val Ile Ser Thr Ala
  921     130                 135                 140
  922 Arg Lys Val Leu Glu Ser Leu Lys Leu Glu Gln Val Leu Gly Lys Glu
  923 145                 150                 155                 160
  924 Gln Thr Pro Gly Ser Lys Gln Val Lys Ala Leu Ile Ser Gln Val Glu
  925             165                 170                 175
  926 Glu Phe Lys Gln Ser Gly Val Leu Thr Ala Ile Pro Thr Pro Gly Thr
  927             180                 185                 190
  928 Asp Leu Ala Ala Thr Ala Arg Val Ala Ser Leu Glu Gln Arg Ile Ser
  929         195                 200                 205
  930 Gln Leu Glu Lys Val Leu Gly Ala Gln Pro Asp Lys Leu Ser Arg Leu
  931     210                 215                 220
```

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932 Thr Ala Ala Thr Asn Thr Thr Asn Val Leu Glu Ala Val Arg His Leu
933 225             230             235                 240
934 Ser Thr Lys Ala Ala Leu Ile Gln Pro Asp Lys Leu Asp Thr Ile Glu
935             245             250                 255
936 Gln Arg Leu Thr Ser Leu Ala Gly Lys Met Asp Ala Ile Ala Glu Lys
937         260             265                 270
938 Ser Ser Gly Ser Ala Gln Asp Ala Lys Arg Asp Gln Lys Ile Thr Glu
939         275             280                 285
940 Leu Tyr Asp Ile Ala Lys Arg Thr Glu Pro Val Val Glu Ile Leu Pro
941     290             295                 300
942 His Val Ile Glu Arg Met Gln Ala Leu Glu Ala Leu His Lys Tyr Ala
943 305             310                 315                 320
944 Asn Asn Phe Ala Lys Ile Ile Ala Glu Ile Glu Gln Lys Gln Gly Thr
945             325             330                 335
946 Ile Thr Thr Ser Leu Val Asn Asn Lys Glu Leu Leu His Ser Val Gln
947         340             345                 350
948 Glu Thr Phe Ala Gln Asn Leu Glu Thr Ile Asn Ser Lys Val Ala Lys
949         355             360                 365
950 Val Glu Gln Arg Val Ala Ala Ile Ser Ser Ala Lys
951     370             375                 380
E--> 953 W:\DOCS\BGY\SEQUENCE LISTING\UC Sequences\UC069.001A.doc
E--> 954 051801
E--> 955 1
E--> 957 1
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delete at end of file

see following pages for more error